In the Specification

Please amend the paragraph beginning at page 17, line 6, as follows:

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by the National Center for Biotechnology Information ~~NCBI~~ (NCBI, Bethesda, Maryland) that can be obtained through the internet ~~(ftp:/ncbi.nlm.nih.gov/pub/)~~. Exemplary tools include the BLAST system available at the NCBI website ~~http://wwww.ncbi.nlm.nih.gov~~. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained using the ~~MacVetor~~ MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

Please amend the paragraph beginning at page 84, line 17, as follows:

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (*see, e.g.,* Parker et al, *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health ~~World Wide Web~~ website ~~at URL http://bimas.dcrt.nih.gov~~. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).